

SEQUENCE LISTING

<110> French, Cynthia K.
Schneider, Patrick A.
Yamamoto, Karen K.

<120> Prostate Cancer-Specific Marker

<130> 107-206-C

<140> to be assigned
<141> 2000-10-04

<150> 60/041,246
<151> 1997-03-07

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<151> 1997-05-15

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<170> PatentIn Ver. 2.1

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Met Ala Pro Ile Thr Thr Ser Arg

gaa gaa ttt gat gaa atc ccc aca gtg gtg ggg atc ttc agt gca ttt 222
 Glu Glu Phe Asp Glu Ile Pro Thr Val Val Gly Ile Phe Ser Ala Phe

10 15 20

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 Gly Leu Val Phe Thr Val Ser Leu Phe Ala Trp Ile Cys Cys Gln Arg
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aaa tca tcc aag tct aac aag act cct cca tac aag ttt gtg cat gtg 318
 Lys Ser Ser Lys Ser Asn Lys Thr Pro Pro Tyr Lys Phe Val His Val
 45 50 55

ctt aag gga gtt gat att tac cct gaa aac cta aat agc aaa aag aag 366
 Leu Lys Gly Val Asp Ile Tyr Pro Glu Asn Leu Asn Ser Lys Lys Lys
 60 65 70

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 Phe Gly Ala Asp Asp Lys Asn Glu Val Lys Asn Lys Pro Ala Val Pro
 75 80 85

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 Lys Asn Ser Leu His Leu Asp Leu Glu Lys Arg Asp Leu Asn Gly Asn
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 Ala Thr Pro Lys Leu Phe Leu Glu Gly Glu Lys Glu Ser Val Ser Pro
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 Glu Ser Leu Lys Ser Ser Thr Ser Leu Thr Ser Glu Glu Lys Gln Glu
 140 145 150

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 Lys Leu Gly Thr Leu Phe Phe Ser Leu Glu Tyr Asn Phe Glu Arg Lys
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Pro Ala Phe Asp Glu Thr Phe Thr Phe Tyr Gly Ile Pro Tyr Thr Gln				
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Ser Arg Asp Asp Ile Ile Gly Glu Val Leu Ile Pro Leu Ser Gly Ile				
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Asn Val Arg Lys Ser Ser Gly Arg Gly Glu Leu Leu Ile Ser Leu Cys				
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Tyr Gln Ser Thr Thr Asn Thr Leu Thr Val Val Val Leu Lys Ala Arg				
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cat ctg cct aaa tct gat gtg tcc gga ctt tca gat ccc tat gtc aaa				1134
His Leu Pro Lys Ser Asp Val Ser Gly Leu Ser Asp Pro Tyr Val Lys				
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Val Asn Leu Tyr His Ala Lys Lys Arg Ile Ser Lys Lys Thr His				
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35 40 45

Pro Pro Tyr Lys Phe Val His Val Leu Lys Gly Val Asp Ile Tyr Pro
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Glu Asn Leu Asn Ser Lys Lys Phe Gly Ala Asp Asp Lys Asn Glu
65 70 75 80

Val Lys Asn Lys Pro Ala Val Pro Lys Asn Ser Leu His Leu Asp Leu
85 90 95

Glu Lys Arg Asp Leu Asn Gly Asn Phe Pro Lys Thr Asn Leu Lys Pro
100 105 110

Gly Ser Pro Ser Asp Leu Glu Asn Ala Thr Pro Lys Leu Phe Leu Glu
115 120 125

Gly Glu Lys Glu Ser Val Ser Pro Glu Ser Leu Lys Ser Ser Thr Ser
130 135 140

Leu Thr Ser Glu Glu Lys Gln Glu Lys Leu Gly Thr Leu Phe Phe Ser
145 150 155 160

Leu Glu Tyr Asn Phe Glu Arg Lys Ala Phe Val Val Asn Ile Lys Glu
165 170 175

Ala Arg Gly Leu Pro Ala Met Asp Glu Gln Ser Met Thr Ser Asp Pro
180 185 190

Tyr Ile Lys Met Thr Ile Leu Pro Glu Lys Lys His Lys Val Lys Thr
195 200 205

Arg Val Leu Arg Lys Thr Leu Asp Pro Ala Phe Asp Glu Thr Phe Thr

210

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Phe Tyr Gly Ile Pro Tyr Thr Gln Ile Gln Glu Leu Ala Leu His Phe
225 230 235 240

Thr Ile Leu Ser Phe Asp Arg Phe Ser Arg Asp Asp Ile Ile Gly Glu
245 250 255

Val Leu Ile Pro Leu Ser Gly Ile Glu Leu Ser Glu Gly Lys Met Leu
260 265 270

Met Asn Arg Glu Ile Ile Lys Arg Asn Val Arg Lys Ser Ser Gly Arg
275 280 285

Gly Glu Leu Leu Ile Ser Leu Cys Tyr Gln Ser Thr Thr Asn Thr Leu
290 295 300

Thr Val Val Val Leu Lys Ala Arg His Leu Pro Lys Ser Asp Val Ser
305 310 315 320

Gly Leu Ser Asp Pro Tyr Val Lys Val Asn Leu Tyr His Ala Lys Lys
325 330 335

Arg Ile Ser Lys Lys Thr His Val Lys Lys Cys Thr Pro Asn Ala
340 345 350

Val Phe Asn Glu Leu Phe Val Phe Asp Ile Pro Cys Glu Gly Leu Glu
355 360 365

Asp Ile Ser Val Glu Phe Leu Val Leu Asp Ser Glu Arg Gly Ser Arg
370 375 380

Asn Glu Val Ile Gly Gln Leu Val Leu Gly Ala Ala Ala Glu Gly Thr
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Gly Gly Glu His Trp Lys Glu Ile Cys Asp Tyr Pro Arg Arg Gln Ile
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Ala Lys Trp His Val Leu Cys Asp Gly
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35 40 45

Pro Pro Tyr Lys Phe Val His Val Leu Lys Gly Val Asp Ile Tyr Pro
50 55 60

Glu Asn Leu Ser Ser Lys Lys Phe Gly Gly Asp Asp Lys Ser Glu
65 70 75 80

Ala Lys Arg Lys Ala Ala Leu Pro Asn Leu Ser Leu His Leu Asp Leu

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90

95

Glu Lys Arg Asp Leu Asn Gly Asn Phe Pro Lys Thr Asn Pro Lys Ala
100 105 110

Gly Ser Ser Ser Asp Leu Glu Asn Val Thr Pro Lys Leu Phe Pro Glu
115 120 125

Thr Glu Lys Glu Ala Val Ser Pro Glu Ser Leu Lys Ser Ser Thr Ser
130 135 140

Leu Thr Ser Glu Glu Lys Gln Glu Lys Leu Gly Thr Leu Phe Leu Ser
145 150 155 160

Leu Glu Tyr Asn Phe Glu Lys Ala Phe Val Val Asn Ile Lys Glu
165 170 175

Ala Gln Gly Leu Pro Ala Met Asp Glu Gln Ser Met Thr Ser Asp Pro
180 185 190

Tyr Ile Lys Met Thr Ile Leu Pro Glu Lys Lys His Lys Val Lys Thr
195 200 205

Arg Val Leu Arg Lys Thr Leu Asp Pro Val Phe Asp Glu Thr Phe Thr
210 215 220

Phe Tyr Gly Val Pro Tyr Pro His Ile Gln Glu Leu Ser Leu His Phe
225 230 235 240

Thr Val Leu Ser Phe Asp Arg Phe Ser Arg Asp Asp Val Ile Gly Glu
245 250 255

Val Leu Val Pro Leu Ser Gly Ile Glu Leu Ser Asp Gly Lys Met Leu
260 265 270

Met Thr Arg Glu Ile Ile Lys Arg Asn Ala Lys Ser Ser Gly Arg
275 280 285

Gly Glu Leu Leu Val Ser Leu Cys Tyr Gln Ser Thr Thr Asn Thr Leu
290 295 300

Thr Val Val Val Leu Lys Ala Arg His Leu Pro Lys Ser Asp Val Ser
305 310 315 320

Gly Leu Ser Asp Pro Tyr Val Lys Val Asn Leu Tyr His Ala Lys Lys
325 330 335

Arg Ile Ser Lys Lys Thr His Val Lys Lys Cys Thr Pro Asn Ala

340

345

350

Val Phe Asn Glu Leu Phe Val Phe Asp Ile Pro Cys Glu Ser Leu Glu
355 360 365

Glu Ile Ser Val Glu Phe Leu Val Leu Asp Ser Glu Arg Gly Ser Arg
370 375 380

Asn Glu Val Ile Gly Arg Leu Val Leu Gly Ala Thr Ala Glu Gly Ser
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Ala Lys Trp His Met Leu Cys Asp Gly
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<213> Homo sapiens

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Ile Lys Glu Gly Arg Asn Leu Ile Pro Met Asp Pro Asn Gly Leu Ser
35 40 45

Asp Pro Tyr Val Lys Val Lys Leu Ile Pro Asp Asp Lys Asp Gln Ser
50 55 60

Lys Lys Lys Thr Arg Thr Thr Lys Ala Cys Leu Asn Pro Val Trp Asn
65 70 75 80

Glu Thr Leu Thr Tyr Asp Leu Lys Pro Glu Asp Lys Asp Arg Arg Ile
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Gly Ala Leu Ser Phe
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<223> Repro-PC-1.0 (PC-20) "B" internal repeat (amino acid) positions 276-397

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20 25 30

Val Leu Lys Ala Arg His Leu Pro Lys Ser Asp Val Ser Gly Leu Ser
35 40 45

Asp Pro Tyr Val Lys Val Asn Leu Tyr His Ala Lys Lys Arg Ile Ser
50 55 60

Lys Lys Lys Thr His Val Lys Lys Cys Thr Pro Asn Ala Val Phe Asn
65 70 75 80

Glu Leu Phe Val Phe Asp Ile Pro Cys Glu Gly Leu Glu Asp Ile Ser
85 90 95

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100 105 110

Ile Gly Gln Leu Val Leu Gly Ala Ala
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20 25 30

Leu Lys Lys Met Asp Val Gly Gly Leu Ser Asp Pro Tyr Val Lys Ile
35 40 45

His Leu Met Gln Asn Gly Lys Arg Leu Lys Lys Lys Lys Thr Thr Ile
50 55 60

Lys Lys Asn Thr Leu Asn Pro Tyr Tyr Asn Glu Ser Phe Ser Phe Glu
 65 70 75 80

Val Pro Phe Glu Gln Ile Gln Lys Val Gln Val Val Val Thr Val Leu
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Asp Tyr Asp Lys Ile Gly Lys Asn Asp Ala Ile Gly Lys Val Phe Val
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Gly Tyr Asn
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20 25 30

Ala Ala Glu Leu Pro Ala Leu Asp Met Gly Gly Thr Ser Asp Pro Tyr
35 40 45

Val Lys Val Phe Leu Leu Pro Asp Lys Lys Lys Lys Phe Glu Thr Lys
50 55 60

Val His Arg Lys Thr Leu Asn Pro Val Phe Asn Glu Gln Phe Thr Phe
65 70 75 80

Lys Val Pro Tyr Ser Glu Leu Gly Gly Lys Thr Leu Val Met Ala Val
85 90 95

Tyr Asp Phe Asp Arg Phe Ser Lys His Asp Ile Ile Gly Glu Phe Lys
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Val Pro Met Asn Thr Val Asp Phe
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20 25 30

Ala Met Asp Glu Gln Ser Met Thr Ser Asp Pro Tyr Ile Lys Met Thr
35 40 45

Ile Leu Pro Glu Lys Lys His Lys Val Lys Thr Arg Val Leu Arg Lys
50 55 60

Thr Leu Asp Pro Ala Phe Asp Glu Thr Phe Thr Phe Tyr Gly Ile Pro
65 70 75 80

Tyr Thr Gln Ile Gln Glu Leu Ala Leu His Phe Thr Ile Leu Ser Phe
85 90 95

Asp Arg Phe Ser Arg Asp Asp Ile Ile Gly Glu Val Leu Ile Pro Leu
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<211> 9

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<223> residue 2=Asp, Glu, Ala, Ser or Thr

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<212> PRT

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<223> residue 2=Asp, Glu, Ala, Ser or Thr

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Cys, Gly, Asp or Glu

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Cys, Gly, Asp or Glu

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<223> residue 9=Phe, Ile, Trp, Met or Leu

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Gly Ala

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<210> 24

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20 25 30

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Arg Phe Ser Arg Asp Asp Ile Ile Gly Glu Val Leu
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<213> Homo sapiens

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<210> 26

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<212> PRT

<213> Homo sapiens

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Val Leu Asp Ser Glu Arg Gly Ser Arg Asn Glu Val Ile Gly Gln Leu
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<220>

<223> residue 5=Val or Ile

<400> 27

Ser Asp Pro Tyr Xaa Lys
1 5